09/988384 STN Search Summary

=> d his

L1 L2 L3 L4 L5 L6 L7 L8	41 S L1 A 37 S L1 (HYMYCI ND (PC P) (PC S) (PC ND VEN ND PRC ND GEN ND POI	IN OR PIKROMYCI DLYKETIDE (2W) DLYKETIDE (2W) DLYKETIDE (2W) NEZUELAE DMOTER NE LYKETIDE	N OR PICROMYCIN OF SYNTHASE) SYNTHASE)	R NARBOMYCIN
L6	ANSWER 1 OF 3 CA		COPYRIGHT 2004	ACS on STN	
AN TI	2000:756845 CAPL A method for prep peptides using co functional domain	aring mbina	tions of plasmi	s of polyketides ds carrying genes	and non-ribosomal for different
IN PA	Santi, Daniel V.; Kosan Biosciences	Xue,	Qun; Ashley, G		
SO	PCT Int. App1., 3	32 pp.		anni Tarmiov, No	D.2.00
	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
ΡI	wo 2000063361 wo 2000063361	A2 A3	20001026 20010712	WO 2000-US10021	20000412
	EP 11/71583	A3 A2	20010712	EP 2000-922192	20000412
	JP 2⁄003504006	Т2	20030204	JP 2000-612440	20000412
PRAI	US/1999-129731P	P	19990416		•
	₩Ø 2000-US10021	M	20000412	4	
L6 AN TI	1999:764178 CAPI Sequence and reco	LUS omb i na		ACS on STN polyketide syntha	
	antibiotics				
IN	Ashley, Gary; Bet Li	lach,	Melanie C.; Be	etlach, Mary; McDa	niel, Robert; Tang,
PA	Kosan Biosciences		., USA		
SO	PCT Int. Appl., 9	KIND	DATE	APPLICATION NO.	DATE
PI .	WO 9961599	A2 .	19991202	WO 1999-US11814	19990527
	WO 9961599	A3	20000127		
	∕US 6503741	В1	20030107	US 1998-141908	19980828
	CA 2328427	AA	19991202	CA 1999-2328427	19990527 19990527
	AU 9942137 AU 762399	A1 B2	19991213 20030626	AU 1999-42137	19990527
	EP 1082439.	В2 A2	20030020	EP 1999-925954	19990527
	JP 2002516090	T2	20020604	JP 2000-550984	19990527
	NZ 509006	A	20030926	NZ 1999-509006	19990527
PRAI		P ·	19980528		
	US 1998-141908	A	19980828		
	US 1998-100880P	Р.	19980922		
	US 1999-119139P	P	19990208		
	WO 1999-US11814	W	19990527		

```
L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
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AN 1997:501482 CAPLUS

TI Polyhydroxyalkanoate synthase recombinant production and novel pathway for polyhydroxyalkanoate synthesis

IN Sherman David H.; Williams, Mark D.; Xue, Yongquan

PA Regents of the University of Minnesota, USA; Sherman, David H.; Williams, Mark D.; Xue, Yongquan

SO	PCT Int. Appl.,	90 pp.			
	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PΙ	WO 9722711	A1	19970626	WO 1996-US20119	19961218
	EP 870053	A1	19981014	EP 1996-944849	19961218
	JP 2000502256	T2	20000229	JP 1997-522970	19961218
	US 6600029	Ŗ1	20030729	US 1998-91609	19980619
PRAI	US 1995-8847P	P _.	19951219	•	
	WO 1996-US20119	M	19961218		

- L9 ANSWER 2 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 2003:435232 CAPLUS

US 2001-793708

- TI Engineering of recombinant Streptomyces venezuelae narbonolide polyketide synthase for production of novel polyketide products
- IN Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
 Li
- PA USA
- SO U.S. Pat. Appl. Publ., 74 pp., Cont.-in-part of U.S. Ser. No. 657,440.

 PATENT NO KIND DATE APPLICATION NO. DATE

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ΡI	US	2003104597	A1	20030605	US	2001-793708	20010222
	US	2002034797	A1	20020321	US	1997-846247	19970430
	US.	6391594	В2	20020521			
	US	6558942	В1	20030506	US	1998-73538	19980506
	US	6503741	В1	20030107	US	1998-141908	19980828
	US	6117659	A	20000912	US	1999-320878	19990527
	US	6509455	В1	20030121	US	2000-657440	20000907
	WO	2002097062	A2	20021205	WO	2002-US5642	20020222
	US	2003162262	A1	20030828	US	2002-160539	20020529
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	US	1999-134990P	P	19990520		•	
	US	1999-320878	A	19990527			
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	US	1994-238811	A2	19940506			
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20010222

Α

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ANSWER 4 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
     2002:927567 CAPLUS
AN
     Recombinant narbonolide polyketide synthase for the production of
TI
     polyketides useful as antibiotics
     Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
, IN
     Kosan Biosciences, Inc., USA
PΑ
SO
     PCT Int. Appl., 127 pp.
                                            APPLICATION NO.
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     US 1999-134990P
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     US 2000-657440
                        Α2
                             20000907
     ANSWER 6 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
L9 ·
     2002:276140 CAPLUS
ΑN
     Recombinant bacteria producing substances with altered sugar moieties and
TΙ
     their use for production of these substances
     Liu, Hung-Wen; Sherman, David H.; Zhao, Lishan
IN
     Regents of the University of Minnesota, USA
PA
SO
     PCT Int. Appl., 174 pp.
                       KIND DATE
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PI
     WO 2002029035
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                                                              20011005
     EP 1325134
                        A2
                             20030709
PRAI US 2000-238185P
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     WO 2001-US31255
                        W -
                             20011005
     ANSWER 8 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
1.9
ΑN
     2001\392662 CAPLUS
     Characterization and analysis of the PikD regulatory factor in the
TТ
     pikromycin biosynthetic pathway of Streptomyces venezuelae
     Wilśon \ Daniel J.; Xue, Yongquan; Reynolds, Kevin A.; Sherman, David H.
ΑU
      Journal of Bacteriology (2001), 183(11), 3468-3475
SO
                                 June
     ANSWER 9 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
L9
      2001:127810 CAPLUS
ΑN
     The Streptomyces venezuelae pikAV gene contains a
TТ
      transcription unit essential for expression of enzymes involved in
      glycosylation of narbonolide and 10-deoxymethynolide
     Chen, S.; Roberts, J. B.; Xue, Y.; Sherman, D. H.; Reynolds, K. A.
ΑU
```

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SO

Gene (2001), 263(1-2), 255-264

Jan

3

- L9 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 2001:79736 CAPLUS
- TI Biosynthesis and combinatorial biosynthesis of pikromycin -related macrolides in Streptomyces venezuelae
- AU Xue, Yongquan; Sherman, David H.
- SO Metabolic Engineering (2001), 3(1), 15-26
- L9 ANSWER 13 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 2000:152485 CAPLUS
- TI Genetic architecture of the polyketide synthases for methymycin and pikromycin series macrolides
- AU Xue, Y.; Wilson, D.; Sherman, D. H.
- SO Gene (2000), 245(1), 203-211
- L9 ANSWER 14 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 2000:15381 CAPLUS
- TI Gene clusters encoding proteins involved in methymycin and pikromycin and desosamine biosynthesis from Streptomyces venezuelae
- IN Sherman, David H.; Liu, Hung-Wen; Xue, Yongquan; Zhao, Lishan
- PA Regents of the University of Minnesota, USA
- SO PCT Int. Appl., 438 pp.

50	PC.	i int. Appi.,	430 pp	•	
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ΡI	WO	2000000620	A2	20000106	WO 1999-US14398 19990625
	WO	2000000620	А3	20000413	
	US	6265202	В1	20010724	US 1998-105537 19980626
	ΑU	9947199	A1	20000117	AU 1999-47199 19990625
	ΕÉ	1090125	A2	20010411	EP 1999-930718 19990625
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	US	2003073824	A1	20030417	US 2001-988384 20011119
PRAI	US	1998-105537	A2	19980626	
	WO	1999-US14398	W	19990625	•

- L9 ANSWER 15 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 1999:764178 CAPLUS
- TI Sequence and recombinant narbonolide polyketide synthase applications from Streptomyces venezuelae for creation of useful antibiotics
- IN Ashley, Gary; Betlach, Melanie C.; Betlach, Mary; McDaniel, Robert; Tang,
- SO PCT Int. Appl., 98 pp.

PI WO 9961599 A2 19991202 WO 1999-US11814 19990527 WO 9961599 A3 20000127 CX 6503741 B1 20030107 US 1998-141908 19980828 CA 2328427 AA 19991202 CA 1999-2328427 19990527 AU 9942137 A1 19991213 AU 1999-42137 19990527 AU 762399 B2 20030626 EP 1082439 A2 20010314 EP 1999-925954 19990527FI JP 2002516090 T2 20020604 JP 2000-550984 19990527 NZ 509006 A 20030926 NZ 1999-509006 19990527 PRAI US 1998-87080P P 19980528 US 1998-141908 A 19980828 US 1998-100880P P 19980922	30	PATENT NO.	KIND	DATE	. APPLICATION NO.	DATE
US 6503741 B1 20030107 US 1998-141908 19980828 CA 2328427 AA 19991202 CA 1999-2328427 19990527 AU 9942137 A1 19991213 AU 1999-42137 19990527 AU 762399 B2 20030626 EP 1082439 A2 20010314 EP 1999-925954 19990527FI JP 2002516090 T2 20020604 JP 2000-550984 19990527 NZ 509006 A 20030926 NZ 1999-509006 19990527 PRAI US 1998-87080P P 19980528 US 1998-141908 A 19980828	ΡI	WO 9961599	A2	19991202	WO 1999-US11814	19990527
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US 1998-100880P P 19980922		US 1998-14190	B A	19980828		
		US 1998-10088	OP P	19980922		
US 1999-119139P P 19990208		US 1999-11913	9P P	19990208		
WO 1999-US11814 W ,19990527		WO 1999-US118	14 W	,19990527	•	

- L9 ANSWER 17 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 1999:548433 CAPLUS
- TI Elucidating the mechanism of chain termination switching in the picromyc; methymycin polyketide synthase
- AU Tang, LA; \Fu, Hong; Betlach, Melanie C.; McDaniel, Robert
- SO Chemistry & Biology (1999), 6(8), 553-558
- L9 ANSWER 20 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 1998:801,708 CAPLUS
- TI Hydroxylation of macrolactones YC-17 and narbomycin is mediated by the pike-encoded cytochrome P450 in Streptomyces venezuelae
- AU Xue, Yongquan; Wilson, Daniel; Zhao, Lishan; Liu, Hung-Wen; Sherman, David H.
- SO Chemistry & Biology (1998), 5(11), 661-667
- L9 ANSWER 21 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
 - / 1998:679770 CAPLUS
 - A gene cluster for macrolide antibiotic biosynthesis in Streptomyces venezuelae: architecture of metabolic diversity
- AU Xue, Yongquan; Zhao, Lishan; Liu, Hung-Wen; Sherman, David H.
- SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(21), 12111-12116
- L9 ANSWER 22 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 1998:624/68 CAPLUS
- TI Characterization of the macrolide P-450 hydroxylase from Streptomyces venezuelae which converts narbomycin to picromycin
- AU Betlach Melanie C.; Kealey, James T.; Betlach, Mary C.; Ashley, Gary W.; McDarie, Robert
- SO Biochemistry (1998), 37(42), 14937-14942
- L9. ANSWER 25 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 1997:501482 CAPLUS
- TI Polyhydroxyalkanoate synthase recombinant production and novel pathway for polyhydroxyalkanoate synthesis
- IN Sherman, David H.; Williams, Mark D.; Xue, Yongquan
- PA Regents of the University of Minnesota, USA; Sherman, David H.; Williams, Mark D.; Xue, Yongquan
- SO PCT Int. Appl., 90 pp.

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	EP 870053	A1	19981014	EP 1996-944849	19961218
	JP 2000502256	Τ2	20000229	JP 1997-522970	19961218
	US 6600029	B1	20030729	US 1998-91609	19980619
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(without alignments)

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Post-processing: Minimum Match 0%

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em mu:*

em_om:*
em_or:*

em_ov:*

em_pat:*

em_ph:*

em_pl:*

em ro:*

em sts:*

Maximum Match 100%

Listing first 45 summaries

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}

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 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em htg other:*
 33: em htg mus:*
 34: em_htg_pln:*
      em_htg_rod:*
 35:
 36:
      em htg mam:*
      em_htg_vrt:*
em_sy:*
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 38:
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	3	405.8	13.9	834	6	AX698015	AX698015 Sequence
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С	5	346.4	11.9	36270	1	SLLINC	X79146 S.lincolnen
	6	324.2	11.1	1446	1	SLLMRBG	X62867 S.lincolnen
	7	247.8	8.5	1348	6	E07944	E07944 Mycinomycin
	. 8	247.8	8.5	2148	1	MPUMYRB	D14532 M.griseorub
	9	221.6	7.6	1163	1	AF462611	AF462611 Micrococc
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С	11	197.4	6.8	2148	1	MPUMYRB	D14532 M.griseorub
С	12	179.2	6.2	15100	1	AF492560	AF492560 Corynebac
Ċ	13	178.8	6.1	834	6	AX698015	AX698015 Sequence
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	15	176.6	6.1	89'90	1	CXU21300	U21300 Corynebacte
C	16	176.6	6.1	51409	1	AF024666	AF024666 Corynebac
	17	176	6.0	1810	1	NG2MET	M36726 Plasmid pNG
	18	176	6.0	3123	1	AF338705	AF338705 Corynebac
	19	175	6.0	1517	1	CDERMA	X51472 Corynebacte
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	21	175	6.0	4524	1	AF411029	AF411029 Propionib
	22	171.6	5.9	2198	1	AF338706	AF338706 Corynebac
	.23	164.4	5.6	36270	1	SLLINC	X79146 S.lincolnen
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С	27	144.4	5.0	1517	1	CDERMA	X51472 Corynebacte
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(without alignments)

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Post-processing: Minimum Match 0%

Maximum Match 100%

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7 June 1 / Grand 1 / Grand

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

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		•	%				
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~		360		37948	21	AAZ87285	S. venezuelae maci S. venezuelae pik
С	5		12.4				
	6	247.8	8.5	1348	15	AAQ67407	MyrB gene DNA, enc
С	7	197.4	6.8	1348	15	AAQ67407	MyrB gene DNA, enc
С	8	185.2	6.4	969	21	AAZ87296	S. venezuelae macr
	9	185.2	6.4	1011	21	AAZ87295	S. venezuelae macr
С	10	185.2	6.4	36778	21	AAZ87318	S. venezuelae pik
	11	134.6		114955	20	AAX53491	Human adenosine A1
C	12	132.2	4.5	1260		AAN81457	carB Gene sequence
C	13	129.4		114955	20	AAX53491	Human adenosine Al
	14	115	4.0	1260		AAN81457	carB Gene sequence
	15	86.8		154746	24	AAD25519	Human herpesvirus
С	16	86.8		154746	24	AAD25519	Human herpesvirus
	17	84.6	2.9	5760	24	ABS78661	M. echinospora DNA
C	18	82.2	2.8	3957	22	AAA09686	HSV-2 immediate ea
	19	81.8	2.8	15239	17	AAT33536	BCG deletion regio
С	20	81.8	2.8	4403765	22	AAI99683	Mycobacterium tube
С	21	81.8	2.8	4411529	22	AAI99682	Mycobacterium tube
	22	81.4	2.8	1127	21	AAA02477	Human colon cancer
	23	80.4	2.8	3957	22	AAA09686	HSV-2 immediate ea
С	24	79.6	2.7	5877	24	ABS78681	Kitasatosporia sp.
	25	78.4	2.7	1459	21	AAA02528	Human colon cancer
	26	78.4	2.7	12733	24	ABK98631	Vector pEPEF14 con
	27	78.4	2.7	12739	24	ABK98592	Vector pEPEF1 cont
C	28	77	2.6	1337	20	AAZ17263	Human gene express
	29	75.8	2.6	88421	24	AAL40781	88421nt genomic DN
	30	75.6	2.6	109519	22	ÀAS08693	Micromonospora DNA
	31	74.2	2.5	2561	22	AAH26500	Rabbit low density
С	32	72.4	2.5	58857	21	AAA58471	Nucleotide sequenc
C	33	71.6	2.5	8438	15	AAQ73500	DNA encoding Pseud
	34	71.6	2.5	12001	16	AAQ76213	HSV L/ST region.
Ċ	35	71.2	2.4	42999	24	ABS65032	Invertebrate forag
	36.	71	2.4	712	24	ABQ40858	Oligonucleotide fo
C	37	71	2.4	712	24	ABQ40859	Oligonucleotide fo
	38	70.6	2.4		22	AAI99682	Mycobacterium tube
С	39	70.2		109519	22	AAS08693	Micromonospora DNA
c	40	70.2		125401	22	AAD17186	Streptomyces nours
C	41	69.4	2.4	2721	12	AAQ10212	BamHI J-I fragment
c	42	69.4	2.4	2721	12	AAQ10543	BamHI J-I fragment
0	43	69.2	2.4	594	24	ABQ43958	Oligonucleotide fo
С	44	69.2	2.4	594	24	ABQ43959	Oligonucleotide fo
0	45	69		4403765	22	AAI99683	Mycobacterium tube
	10	0,0	۷.4	1100100	2.2	111111	Mycobacterrum tube

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 00:31:29; Search time 165 Seconds

(without alignments)

7787.068 Million cell updates/sec

Title: SEQ5-1-2911

Perfect score: 2911

Sequence: 1 gggdccctcctcacgcgtct.....gcttccggagacggagccgg 2911

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:*

1: /cgn2 6/ptodata/2/ina/5A COMB.seq:*

2: /cgn2 6/ptodata/2/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*

4: /cgn2 6/ptodata/2/ina/6B COMB.seq:*

5: /cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*

6: /cgn2 6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ult No.	Score	% Query Match	Length	DВ	ID	Description
	1	1741	59.8	36778	3	US-09-105-537-5	Sequence 5, Appli
C	2	1011	34.7	1011	3	US-09-105-537-26	Sequence 26, Appl
	3	185.2	6.4	1011	3	US-09-105-537-26	Sequence 26, Appl
С	4	185.2	6.4	36778	3	US-09-105-537-5	Sequence 5, Appli
	5	81.8	2.8	15239	1	US-08-390-878-17	Sequence 17, Appl
С	6	81.8	2.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C	7	81.8	2.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
С	8	71.6	2.5	8438	1	US-07-945-283-1	Sequence 1, Appli
	9	70.6	2.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	10	70	2.4	12001	1	US-08-458-568A-11	Sequence 11, Appl
С	11	69.4	2.4	2721	6	5215881-2	Patent No. 5215881
	12	69	2.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 03:12:10; Search time 1600 Seconds

(without alignments)

6412.866 Million cell updates/sec

Title: SE05-1-2911

Perfect score: 2911

1 gggcccctcctcacgcgtct.....gcttccggagacggagccqg 2911 Sequence:

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2324096 segs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB sed length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications NA:* Database :

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/cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*

/cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

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/cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

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/cgn2 6/ptodata/1/pubpna/US08 NEW PUB.seq:* 7:

/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

/cgn2 6/ptodata/1/pubpna/US09A PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US09B PUBCOMB.seg:*

11: /cgn2 6/ptodata/1/pubpna/US09C PUBCOMB.seg:*

12: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

13: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq2:*

/cgn2 6/ptodata/1/pubpna/US10A PUBCOMB.seq:* 14:

/cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq:* 15:

/cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:* 16: 17:

/cgn2 6/ptodata/1/pubpna/US60 NEW PUB.seq:* /cgn2 6/ptodata/1/pubpna/US60 PUBCOMB.seq:* 18:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Result Query Match Length DB ID No. Description Score Sequence 5, Appli US-09-988-384B-5 2911 100.0 37948 11 Sequence 5, Appli 59.8 36778 10 US-09-861-289-5 1741 Sequence 5, Appli 1741 59.8 36778 10 US-09-860-846-5 3 Sequence 5, Appli 1741 59.8 36778 11 US-09-836-821-5 4. 36778 13 US-10-271-889-48 Sequence 48, Appl 59.8 5 1741 34.7 Sequence 26, Appl 1011 10 US-09-861-289-26 С 6 1011 34.7 Sequence 26, Appl 7 1011 1011 10 US-09-860-846-26 С 34.7 1011 11 US-09-988-384B-26 Sequence 26, Appl 8 1011 С 34.7 1011 11 US-09-836-821-26 Sequence 26, Appl 9 1011 С 13 US-10-271-889-26 Sequence 26, Appl 34.7 1011 10 1011 US-09-988-384B-28 969 33.3 969 11 Sequence 28, Appl 11 60196 US-10-205-032-1 Sequence 1, Appli 12 430.6 14.8 15 US-10-205-032-39 Sequence 39, Appl 13 405.8 13.9 834 15 Sequence 5, Appli 12.4 37948 11 US-09-988-384B-5 14 360 Sequence 28, Appl 15 185.2 6.4 969 11 US-09-988-384B-28 1011 10 US-09-861-289-26 Sequence 26, Appl 16 185.2 6.4 185.2 6.4 17 1011 10 US-09-860-846-26 Sequence 26, Appl 185.2 1011 11 US-09-988-384B-26 Sequence 26, Appl 18 6.4 19 185.2 6.4 1011 11 US-09-836-821-26 Sequence 26, Appl 20 185.2 6.4 1011 13 US-10-271-889-26 Sequence 26, Appl 36778 US-09-861-289-5 21 185.2 6.4 10 Sequence 5, Appli C 22 185.2 36778 10 US-09-860-846-5 Sequence 5, Appli 6.4 С 36778 Sequence 5, Appli 23 185.2 6.4 11 US-09-836-821-5 6.4 185.2 36778 13 US-10-271-889-48 Sequence 48, Appl С 24 25 178.8 6.1 834 15 US-10-205-032-39 Sequence 39, Appl С 60196 15 178.8 US-10-205-032-1 Sequence 1, Appli 26 6.1 3.0 154746 13 US-09-827-688-8 Sequence 8, Appli 27 86.8 28 86.8 3.0 154746 13 US-09-827-688-8 Sequence 8, Appli С 11058 29 83.4 2.9 15 US-10-156-761-3629 Sequence 3629, Ap 2.9 9025608 30 83.4 15 US-10-156-761-1 Sequence 1, Appli С Sequence 193, App 82.2 2.8 3957 13 US-10-200-562-193 С 31 Sequence 193, App 32 82.2 2.8 3957 13 US-10-237-551-193 3957 Sequence 193, App 33 80.4 2.8 13 US-10-200-562-193 80.4 2.8 3957 13 US-10-237-551-193 Sequence 193, App 34 78.6 5355 35 2.7 15 US-10-205-032-19 Sequence 19, Appl 36 78.4 2.7 12733 15 US-10-032-393-47 Sequence 47, Appl 37 78.4 2.7 12739 15 US-10-032-393-8 Sequence 8, Appli 38 76.6 2.6 3133 12 US-10-292-798-1191 Sequence 1191, Ap 39 76.6 2.6 3133 13 US-10-017-161-1483 Sequence 1483, Ap 75.8 2.6 88421 10 40 US-09-976-059-1 Sequence 1, Appli 75.2 2.6 1413 15 US-10-156-761-5135 Sequence 5135, Ap 41 42 75.2 2.6 9025608 15 US-10-156-761-1 Sequence 1, Appli 43 74.4 15738 13 US-10-329-079-46 Sequence 46, Appl-2.6 С 61944 13 US-10-329-079-34 44 74.4 2.6 Sequence 34, Appl 45 74.2 2.5 2561 10 US-09-976-740-48 Sequence 48, Appl

ALIGNMENTS

OM nucleic - nucleic search, using sw model

January 14, 2004, 00:17:17; Search time 5853 Seconds Run on:

(without alignments)

12087.875 Million cell updates/sec

Title: SEQ5-1-2911

Perfect score: 2911

1 gggccctcctcacgcgtct.....gcttccggagacggagccgg 2911 Sequence:

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

22781392 seqs, 12152238056 residues Searched:

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:*

1: em_estba:*

2: em_esthum:*

3: em estin:*

4: em estmu:*

5: em estov:*

6: em estpl:*

7: em estro:*

8: em htc:*

9: gb est1:*

10: gb_est2:*

11: gb htc:*

12: qb est3:*

13: qb est4:*

14: gb est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em gss inv:*

19: em gss pln:*

20: em_gss_vrt:*

21: em gss fun:*

22: em_gss_mam:*

23: em gss mus:*

24: em_gss_pro:*

25: em gss rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description Description Description							SUMMARIE	5
No. Score Match Length DB ID Description				8				
c 1 133.6 4.6 1309 29 AG077201 AG077201 Pan trogl c 2 132.8 4.6 1159 29 CC210735 CC210735 CH261-185 c 3 131.6 4.5 1695 29 CC290874 CC2290874 CH261-172 c 4 122.8 4.2 1281 12 B6852363 B6362363 10240401 c 5 120.6 4.1 1188 29 CC199008 CC199008 CC19008 CP461-620 c 6 120.6 4.1 1785 29 CC219555 CC219559 CC219562 C7 P6181-620 c 7 118 4.1 1516 12 B6809984 B6809984 mgC022d c 9 116.4 4.0 1798 29 AG171124 AG171124 AG171124 AG171124 AG17124 AG17124 AG17124 AG171124 AG171124 AG171124 AG171124	Rės	ult		Query				
C 2 132.8 4.6 1159 29 CC210735 CC210735 CC210735 CC210735 CC210735 CC220874 CC290874 CC290874 CC290874 CC290874 CC220874 CC220874 CC210735 CL261-1785 c 4 122.8 4.2 1281 12 Be852363 BG852363 1024034A0 c 5 120.6 4.1 1198 29 CC219595 CC219595 CC219595 CC219595 CC219616-62D c 7 118 4.1 1516 12 B6809984 BG809984 mgc102xd d 116.4 4.0 1798 29 AG171124 AG171124 Pan trog1 c 10 116 4.0 1610 29 B2559386 BZ559386 BZ559386 pac2-164 c 11 114.6 3.9 1299 29 AG033481 AG039481 AG039481 Pan trog1 c 13 114.2 3.9 1121		No.	Score	Mátch	Length	DB	ID	Description
C 2 132.8 4.6 1159 29 CC210735 CC210735 CC210735 CC210735 CC210735 CC220874 CC290874 CC290874 CC290874 CC290874 CC220874 CC220874 CC210735 CL261-1785 c 4 122.8 4.2 1281 12 Be852363 BG852363 1024034A0 c 5 120.6 4.1 1198 29 CC219595 CC219595 CC219595 CC219595 CC219616-62D c 7 118 4.1 1516 12 B6809984 BG809984 mgc102xd d 116.4 4.0 1798 29 AG171124 AG171124 Pan trog1 c 10 116 4.0 1610 29 B2559386 BZ559386 BZ559386 pac2-164 c 11 114.6 3.9 1299 29 AG033481 AG039481 AG039481 Pan trog1 c 13 114.2 3.9 1121								
c 3 131.6 4.5 1695 29 CC290874 CC290874 CC290874 CR261-172 c 4 122.8 4.2 181 12 BG852363 BG852363 BG852363 1024034R0 c 5 120.6 4.1 1198 29 CC190008 CC219595 CC219595 CR261-138 c 6 120.6 4.1 1798 29 CC219595 CC21951 CC21961 Auge CC21961 Auge CC21961 Auge CC21961 Auge CC21961 Auge Auge CC21961 Auge CC21961 Auge Auge<	С	1	133.6	4.6	1309	29	AG077201	
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c 4 122.8 4.2 1281 12 BG852363 BG852363 1024034A0 c 6 120.6 4.1 11785 29 CC190008 CC190008 CC219595 CR261-62D c 7 118 4.1 1516 12 BG809984 BG809984 BG809984 BG804984 Part trog1 12 114.6 3.9 1121 29 AG03220 AG062320 Part trog1 12 114.1 3.8 1250 29 AG043469 AG043469 AG043469 Part trog1 12 11.1 3.8 1651 12 BG809916	С	3 ·	131.6	4.5	1695	29	CC290874	CC290874 CH261-172
c 5 120.6 4.1 1198 29 CC190008 CC190098 CC219595 CH261-62D c 7 118 4.1 1516 12 B6809984 B6809984 mgct002xd c 9 116.4 4.0 1798 29 AG171124 AG171124 AG171124 Part rog1 c 10 116 4.0 1610 29 B2569386 B2569386 B2569386 Pac569386 Pac569381 Pac7144 AG039481 Part rog1 12 14 13.8 3.9 1016 29 MG032484 Pact rog1 AG043469 Pac7679 AG062320 Pact rog1 Pact rog1 AG043469 Pact rog1 Pac76719 AG073481 Pact	С	4			1281	12	BG852363	BG852363 1024034A0
c 6 120.6 4.1 1785 29 CC219595 CC219595 CR261-62D c 7 118 4.1 1516 12 B6809984 BG809984 mgct002xd 8 117 4.0 1798 29 AG171124 AG171124 Pan trogl c 9 116.4 4.0 1610 29 B2569386 B2569386 pacs-2-164 c 11 114.6 3.9 1242 12 BM911414 BM911414 AGENCOURT 12 114.6 3.9 1299 29 AG0339481 AG0339481 Pan trogl c 13 114.2 3.9 1121 29 AG062320 AG062320 Pan trogl c 15 112 3.8 1250 29 AG033469 AG03230 AG0643469 Pan trogl c 16 111.4 3.8 1250 29 AG034469 AG043469 Pan trogl c 16 111.4 3.8 1651 12 B6809816 BG809816 B	С	5			1198	29	CC190008	CC190008 CH261-138
c 7 118 4.1 1516 12 B6809984 BG809984 Mgct002xd c 9 116.4 4.0 1798 29 AG171124 AG171124 Pan trogl c 10 116 4.0 1610 29 B2569386 BZ569386 BZ569386 pacs2-164 c 11 114.6 3.9 1299 29 AG039481 BM911414 BM911414 AGM171124 AG08200 c 13 114.2 3.9 1121 29 AG062320 AG062320 Pan trogl c 15 112 3.8 1250 29 AG043469 AG043469 Pan trogl c 16 11.4 3.8 1251 12 BG809816 BG809816 mgct0001x 17 11.1.4 3.8 1569 29 AG032333 AG032333 AG032338 Pan trogl c 19 110.4 3.8 1569 29 AG033579 AG033679 Pan trogl <					1785	29	CC219595	CC219595 CH261-62D
8 117 4.0 1798 29 AG171124 AG171124 Pan trogl C 9 116.4 4.0 1798 29 AG171124 AG171124 Pan trogl C 10 116 4.0 1610 29 BZ569386 BZ569386 BZ569386 pacs2-164 C 11 114.6 3.9 1242 12 BM911414 BM911414 AGNCOURT 12 114.6 3.9 1299 29 AG033481 AG0339481 Pan trogl 13 114.2 3.9 1016 29 CNS03LU9 AG062320 AG062320 Pan trogl 14 113.8 3.9 1016 29 CNS03LU9 AG043469 AG043469 Pan trogl 15 112 3.8 1250 29 AG043469 AG043469 Pan trogl 16 111.4 3.8 1651 12 BG809816 BG678719 AG032383 Pan trogl 17 111.4 3.8 1651 12 BG809816 BG093383 Pan trogl 18 110.8 3.8 1169 29 AG033579 Pan trogl 20 110.2 3.8 1474 29 BZ569821 BZ569821 BZ569821 BZ569821 BZ569821 BZ569821 BZ569821 BZ569821 B						12	BG809984	BG809984 mgct002xd
c 9 116.4 4.0 1798 29 AG171124 AG171124 Pant trogl c 10 116 4.0 1610 29 BZ569386 BZ678020-14 BM911414 AG039481 Pant trogl c 13 114.6 3.9 129 29 AG039481 AG039481 Pant trogl c 13 114.2 3.9 1016 29 CNS03LU9 AL249930 Tetracdon c 15 112 3.8 1250 29 AG034469 AG043469 Pan trogl c 16 111.4 3.8 1651 12 BG809816 BG809816 BG809816 MG609825 Pan trogl c 19 110.4 3.8 1598 29 AG032383 AG032383 Pan trogl c 1							AG171124	AG171124 Pan trogl
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C 11 114.6 3.9 1242 12 BM911414 AGGNOURT 12 114.6 3.9 1299 29 AG039481 AG039481 Pan trog1 13 114.2 3.9 1121 29 AG062320 AG062320 AG062320 Pan trog1 14 113.8 3.9 1016 29 CNS03LU9 AL249930 Tetraodon c 15 112 3.8 1250 29 AG043469 AG043469 Pan trog1 c 16 111.4 3.8 1651 12 BG809816 BG678719 AGC043469 Pan trog1 17 111.4 3.8 1651 12 BG809816 BG678719 AGC023383 Pan trog1 18 110.8 3.8 1169 29 AG032383 AG032383 Pan trog1 20 110.2 3.8 1474 29 BZ569821 BZ569821 msh2 1034 c 21 109.6 3.8 1122								BZ569386 pacs2-164
12 114.6 3.9 1299 29 AG039481 AG039481 Pan trogl 13 114.2 3.9 1121 29 AG062320 AG062320 Pan trogl 14 113.8 3.9 1016 29 CNS03LU9 AL049930 Tetraodon 15 112 3.8 1250 29 AG043469 AG043469 Pan trogl 16 111.4 3.8 1288 13 BQ678719 BQ678719 AGENCOURT 17 111.4 3.8 1651 12 BG809816 BG809816 mgct001xk AG032383 AG032383 Pan trogl 18 110.4 3.8 1598 29 AG032383 AG030579 Pan trogl 20 110.2 3.8 1474 29 BZ569821 BC2210366 CC231036 CH261-27F AG030611 AG030611 Pan trogl AG043473 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>								
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	L3	\$methymycin or pikromycin or narbomycin	121							
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